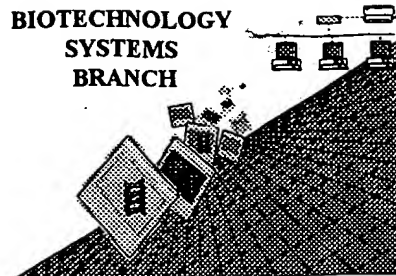


#7

RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/378,045
Source: 1646
Date Processed by STIC: 2/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1646

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/378,045 DATE: 02/05/2001
 TIME: 14:42:54

Input Set : A:\2625-E SeqListing 011801.txt
 Output Set: N:\CRF3\02052001\I378045.raw

**Does Not Comply
 Corrected Diskette Needed**

PS

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2 <110> APPLICANT: Rauch, Charles
3   Walczak, Henning
5 <120> TITLE OF INVENTION: RECEPTOR THAT BINDS TRAIL
7 <130> FILE REFERENCE: 2625-E
9 <140> CURRENT APPLICATION NUMBER: US 09/378,045
10 <141> CURRENT FILING DATE: 1999-08-20
12 <150> PRIOR APPLICATION NUMBER: US 08/883,036
13 <151> PRIOR FILING DATE: 1997-06-26
15 <150> PRIOR APPLICATION NUMBER: US 08/869,852
16 <151> PRIOR FILING DATE: 1997-06-04
18 <150> PRIOR APPLICATION NUMBER: US 08/829,536
19 <151> PRIOR FILING DATE: 1997-03-28
21 <150> PRIOR APPLICATION NUMBER: US 08/815,255
22 <151> PRIOR FILING DATE: 1997-03-12
24 <150> PRIOR APPLICATION NUMBER: US 08/799,861
25 <151> PRIOR FILING DATE: 1997-02-13
27 <160> NUMBER OF SEQ ID NOS: 5
29 <170> SOFTWARE: PatentIn version 3.0/ Microsoft Word, Version 6.0.1
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 1323
33 <212> TYPE: DNA
34 <213> ORGANISM: Homo sapiens
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37 <221> NAME/KEY: CDS
38 <222> LOCATION: (1)..(1323)
40 <400> SEQUENCE: 1
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42 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
43 1          5          10          15
45 agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct ggg ccc      96
46 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
47 20          25          30
49 cgg gtc ccc aag acc ctt gtg etc gtt gtc gcc gcg gtc ctg ctg ttg      144
50 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
51 35          40          45
53 gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct ccc cag      192
54 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
55 50          55          60
57 cag aga gcg gcc cca caa caa aag agg tcc agc ccc tca gag gga ttg      240
58 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
59 65          70          75          80
61 tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc atc tcc      288
62 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
63 85          90          95
65 tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc ctt ttc      336
66 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
67 100         105         110

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RAW SEQUENCE LISTING

DATE: 02/05/2001

PATENT APPLICATION: US/09/378,045

TIME: 14:42:54

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Output Set: N:\CRF3\02052001\I378045.raw

69	tgc	ttg	cgc	tgc	acc	agg	tgt	gat	tca	ggt	gaa	gtg	gag	cta	agt	ccg	384
70	Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	
71		115						120					125				
73	tgc	acc	acg	acc	aga	aac	aca	gtg	tgt	cag	tgc	gaa	gaa	ggc	acc	ttc	432
74	Cys	Thr	Thr	Thr	Arg	Asn	Thr	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	
75		130						135					140				
77	cgg	gaa	gaa	gat	tct	cct	gag	atg	tgc	cgg	aag	tgc	cgc	aca	ggg	tgt	480
78	Arg	Glu	Glu	Asp	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	Gly	Cys	
79	145					150					155					160	
81	ccc	aga	ggg	atg	gtc	aag	gtc	ggt	gat	tgt	aca	ccc	tgg	agt	gac	atc	528
82	Pro	Arg	Gly	Met	Val	Lys	Val	Gly	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile	
83					165					170					175		
85	gaa	tgt	gtc	cac	aaa	gaa	tca	ggt	aca	aag	cac	agt	ggg	gaa	gcc	cca	576
86	Glu	Cys	Val	His	Lys	Glu	Ser	Gly	Thr	Lys	His	Ser	Gly	Glu	Ala	Pro	
87				180					185					190			
89	gct	gtg	gag	gag	acg	gtg	acc	tcc	agc	cca	ggg	act	cct	gcc	tct	ccc	624
90	Ala	Val	Glu	Glu	Thr	Val	Thr	Ser	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Pro	
91		195					200					205					
93	tgt	tct	ctc	tca	ggc	atc	atc	ata	gga	gtc	aca	gtt	gca	gcc	gta	gtc	672
94	Cys	Ser	Leu	Ser	Gly	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val	
95		210				215						220					
97	ttg	att	gtg	gct	gtg	ttt	gtt	tgc	aag	tct	tta	ctg	tgg	aag	aaa	gtc	720
98	Leu	Ile	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys	Val	
99	225					230				235					240		
101	ctt	cct	tac	ctg	aaa	ggc	atc	tgc	tca	ggt	ggt	ggt	ggg	gac	cct	gag	768
102	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly	Asp	Pro	Glu	
103					245					250				255			
105	cgt	gtg	gac	aga	agc	tca	caa	cga	cct	ggg	gct	gag	gac	aat	gtc	ctc	816
106	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	Gly	Ala	Glu	Asp	Asn	Val	Leu	
107					260				265					270			
109	aat	gag	atc	gtg	agt	atc	ttg	cag	ccc	acc	cag	gtc	cct	gag	cag	gaa	864
110	Asn	Glu	Ile	Val	Ser	Ile	Leu	Gln	Pro	Thr	Gln	Val	Pro	Glu	Gln	Glu	
111		275					280					285					
113	atg	gaa	gtc	cag	gag	cca	gca	gag	cca	aca	ggt	gtc	aac	atg	ttg	tcc	912
114	Met	Glu	Val	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly	Val	Asn	Met	Leu	Ser	
115		290					295					300					
117	ccc	ggg	gag	tca	gag	cat	ctg	ctg	gaa	ccg	gca	gaa	gct	gaa	agg	tct	960
118	Pro	Gly	Glu	Ser	Glu	His	Leu	Leu	Glu	Pro	Ala	Glu	Ala	Glu	Arg	Ser	
119	305					310					315				320		
121	cag	agg	agg	agg	ctg	ctg	gtt	cca	gca	aat	gaa	ggt	gat	ccc	act	gag	1008
122	Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Ala	Asn	Glu	Gly	Asp	Pro	Thr	Glu	
123					325					330				335			
125	act	ctg	aga	cag	tgc	ttc	gat	gac	ttt	gca	gac	ttg	gtg	ccc	ttt	gac	1056
126	Thr	Leu	Arg	Gln	Cys	Phe	Asp	Asp	Phe	Ala	Asp	Leu	Val	Pro	Phe	Asp	
127			340					345					350				
129	tcc	tgg	gag	ccg	ctc	atg	agg	aag	ttg	ggc	ctc	atg	gac	aat	gag	ata	1104
130	Ser	Trp	Glu	Pro	Leu	Met	Arg	Lys	Leu	Gly	Leu	Met	Asp	Asn	Glu	Ile	
131			355					360					365				
133	aag	gtg	gct	aaa	gct	gag	gca	gcg	ggc	cac	agg	gac	acc	ttg	tac	acg	1152

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/378,045

DATE: 02/05/2001
 TIME: 14:42:54

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TECH CENTER 16032000

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134 Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr
135      370      375      380
137 atg ctg ata aag tgg gtc aac aaa acc ggg cga gat gcc tct gtc cac      1200
138 Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His
139 385      390      395      400
141 acc ctg ctg gat gcc ttg gag acg ctg gga gag aga ctt gcc aag cag      1248
142 Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln
143      405      410      415
145 aag att gag gac cac ttg ttg agc tct gga aag ttc atg tat cta gaa      1296
146 Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu
147      420      425      430
149 ggt aat gca gac tct gcc atg tcc taa      1323
150 Gly Asn Ala Asp Ser Ala Met Ser
151      435      440
154 <210> SEQ ID NO: 2
155 <211> LENGTH: 440
156 <212> TYPE: PRT
157 <213> ORGANISM: Homo sapiens
159 <400> SEQUENCE: 2
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162 1      5      10      15
164 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
165      20      25      30
167 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
168      35      40      45
170 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
171      50      55      60
174 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
175 65      70      75      80
177 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
178      85      90      95
180 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
181      100      105      110
183 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
184      115      120      125
186 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
187      130      135      140
189 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
190 145      150      155      160
192 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
193      165      170      175
195 Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro
196      180      185      190
198 Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro
199      195      200      205
201 Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
202      210      215      220
204 Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val
205 225      230      235      240

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/378,045
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 TIME: 14:42:54

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207 Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu
208                               245      250      255
210 Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu
211                               260      265      270
213 Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu
214                               275      280      285
216 Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser
217                               290      295      300
219 Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala Glu Arg Ser
220 305                               310      315      320
222 Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp Pro Thr Glu
223                               325      330      335
225 Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp
226                               340      345      350
228 Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile
229                               355      360      365
231 Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr
232                               370      375      380
235 Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His
236 385                               390      395      400
238 Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln
239                               405      410      415
241 Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu
242                               420      425      430
244 Gly Asn Ala Asp Ser Ala Met Ser
245                               435      440
248 <210> SEQ ID NO: 3
249 <211> LENGTH: 157
250 <212> TYPE: DNA
251 <213> ORGANISM: Homo sapiens
253 <220> FEATURE:
254 <221> NAME/KEY: CDS
255 <222> LOCATION: (3)..(155)
257 <220> FEATURE:
258 <221> NAME/KEY: Unsure
259 <222> LOCATION: (145)..(145)
260 <223> OTHER INFORMATION: n = a, t, g, c
262 <220> FEATURE:
263 <221> NAME/KEY: Unsure
264 <222> LOCATION: (149)..(149)
265 <223> OTHER INFORMATION: n = a, t, g, c
268 <400> SEQUENCE: 3
269 ct gag act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg ccc      47
270   Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro
271     1           5           10           15
273 ttt gac tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat      95
274 Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn
275     20           25           30
277 gag ata aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg      143

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/378,045

DATE: 02/05/2001
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278 Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
 279 35 40 45
 W--> 281 tnc acn atg ctg at 157
 W--> 282 Xaa Thr Met Leu
 283 50
 286 <210> SEQ ID NO: 4
 287 <211> LENGTH: 51
 288 <212> TYPE: PRT
 289 <213> ORGANISM: Homo sapiens
 OK--> 290 <400> SEQUENCE: 4
 292 Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe
 293 1 5 10 15
 295 Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu
 296 20 25 30
 W--> 298 Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Xaa
 299 35 40 45
 301 Thr Met Leu
 302 50
 305 <210> SEQ ID NO: 5
 306 <211> LENGTH: 8
 307 <212> TYPE: PRT
 308 <213> ORGANISM: Artificial
 310 <220> FEATURE:
 311 <223> OTHER INFORMATION: FLAG peptide
 313 <400> SEQUENCE: 5
 315 Asp Tyr Lys Asp Asp Asp Asp Lys
 316 1 5

see item 10 on Enn
 Summary
 sheet

VERIFICATION SUMMARY DATE: 02/05/2001
PATENT APPLICATION: US/09/378,045 TIME: 14:42:55

Input Set : A:\2625-E SeqListing 011801.txt
Output Set: N:\CRF3\02052001\I378045.raw

L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:290 M:283 W: Missing Blank Line separator, <400> field identifier
L:298 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:298 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:298 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:298 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:298 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4

Raw Sequence Listing Error Summary

[illegible]

SERIAL NUMBER:

09/328,045

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

RECEIVED

2 Wrapped Aminos

The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".

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3 Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

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4 _____ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 Variable Length

Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences
(OLD RULES)

Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)

Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.

<210> sequence id number

<400> sequence id number

000

10 0 Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism
(NEW RULES)

Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature
(NEW RULES)

Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.